

REMARKS

The Office Action mailed May 13, 2005 has been carefully reviewed and the foregoing amendments are made in response thereto. In view of the amendments and the following remarks, Applicants respectfully request reconsideration and reexamination of this application and the timely allowance of the pending claims.

Preliminary Remark

Applicants note that the Examiner has indicated that claims 57, 58 and 174-177 are allowed and that the rejection of claims 39-53 over McCasky Feazel *et al.* (U.S. Patent No. 6,100,030) in view of DeRisi *et al.* (Science 278:680-686, 1997) and Moyer *et al.* (Applied and Environmental Microbiology 62:2501-2507, 1996) has been withdrawn, thus removing all prior art rejections of claims 39-53.

As suggested by the Examiner, claim 58 has been amended to recite "type IIs endonuclease" in place of "Class IIs endonuclease."

Rejections under 35 USC §112

The Examiner has rejected claims 39-53 as allegedly not being enabled. Applicants respectfully disagree. The Examiner appears to be interpreting claim 39 to require that the computer be used to predict which allelic form or forms of a polymorphism are present in the sample in contrast to what is actually claimed: using a computer to identify polymorphisms (positions where two or more genetically determined alternative sequences or alleles occur in a population) in the subset of fragments that are predicted to be amplified. The computer predicts which polymorphisms will be present in the amplified fragments based on the size of restriction fragments that will be amplified and identification of polymorphic markers that are present in those fragments in one or more human population, using a database of known human polymorphisms. Probes that interrogate the genotype of individual polymorphisms, to determine which allelic form or forms are present in the sample, are then included on the array. The array hybridization pattern would be used to make the empirical determination of which allelic form or forms of a given polymorphism are

present in the sample (the genotype of the sample at that polymorphism). The location of more than one million polymorphisms within the human genome are currently available in public databases and can be searched by position within the genomic sequence using a computer, thus a computer can be used to predict the fragments that will be amplified and to identify polymorphisms within those fragments. Reconsideration and withdrawal of the rejection of claims 39-53 is respectfully requested.

CONCLUSION

For the foregoing reasons, Applicants believe all the pending claims are now in condition for allowance and should be passed to issue. Please deduct any additional fees from, or credit any overpayment to the above-noted Deposit Account. If the Examiner feels that a telephone conference would in any way expedite the prosecution of the application, please do not hesitate to call the undersigned at (408) 731-5768.

Date: August 15, 2005

Respectfully submitted,



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